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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,712

DATE: 10/19/2001

TIME: 11:10:13

Input Set : A:\ES.txt

Output Set: N:\CRF3\10192001\I973712.raw

3 <110> APPLICANT: BOMMARIUS, ANDREAS  
 4 DRAUZ, KARLHEINZ  
 5 VERSECK, STEFAN  
 6 KULA, MARIA-REGINA  
 8 <120> TITLE OF INVENTION: ACETYL AMINO ACID RACEMASE FROM AMYCOLATOPSIS ORIENTALIS FOR  
 RACEMIZING

9 CARBAMOYL AMINO ACIDS  
 11 <130> FILE REFERENCE: 214382US0X  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/973,712  
 C--> 13 <141> CURRENT FILING DATE: 2001-10-11

13 &lt;150&gt; PRIOR APPLICATION NUMBER: DE 10050124.9

14 &lt;151&gt; PRIOR FILING DATE: 2000-10-11

16 &lt;160&gt; NUMBER OF SEQ ID NOS: 2

18 &lt;170&gt; SOFTWARE: PatentIn version 3.1

20 &lt;210&gt; SEQ ID NO: 1

21 &lt;211&gt; LENGTH: 1107

22 &lt;212&gt; TYPE: DNA

23 &lt;213&gt; ORGANISM: Amycolatopsis orientalis

25 &lt;220&gt; FEATURE:

26 &lt;221&gt; NAME/KEY: CDS

27 &lt;222&gt; LOCATION: (1)..(1107)

28 &lt;223&gt; OTHER INFORMATION:

31 &lt;400&gt; SEQUENCE: 1

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33	Val	Lys	Leu	Ser	Gly	Val	Glu	Leu	Arg	Arg	Val	Arg	Met	Pro	Leu	Val	
34	1			5					10					15			
36	gcc	ccg	ttc	cgg	acg	tgc	ttc	ggg	acg	cag	tcc	gag	cgg	gaa	ttg	ctg	96
37	Ala	Pro	Phe	Arg	Thr	Ser	Phe	Gly	Thr	Gln	Ser	Glu	Arg	Glu	Leu	Leu	
38				20				25				30					
40	ctg	gtc	cgc	gcg	gtg	acc	ccg	gcg	ggc	gag	ggc	tgg	ggc	gaa	tgt	gtc	144
41	Leu	Val	Arg	Ala	Val	Thr	Pro	Ala	Gly	Glu	Gly	Trp	Gly	Glu	Cys	Val	
42				35				40				45					
44	gcg	atg	gag	gcg	ccg	ctc	tac	tgc	tgc	gag	tac	aac	gac	gcc	gcc	gac	192
45	Ala	Met	Glu	Ala	Pro	Leu	Tyr	Ser	Ser	Glu	Tyr	Asn	Asp	Ala	Ala	Glu	
46		50					55				60						
48	cac	gtg	ctg	cgg	aac	cat	ctg	atc	ccc	gca	ctg	ctg	gcg	gcc	gag	gac	240
49	His	Val	Leu	Arg	Asn	His	Leu	Ile	Pro	Ala	Leu	Leu	Ala	Ala	Glu	Asp	
50	65				70					75				80			
52	gtg	acc	gcg	cac	aag	gtg	acg	ccg	ttg	ctg	gcg	aag	ttc	aag	ggc	cac	288
53	Val	Thr	Ala	His	Lys	Val	Thr	Pro	Leu	Leu	Ala	Lys	Phe	Lys	Gly	His	
54				85				90				95					
56	cgg	atg	gcg	aag	ggc	gcg	ctg	gag	atg	gcg	gtc	ctc	gac	gcc	gaa	ctc	336
57	Arg	Met	Ala	Lys	Gly	Ala	Leu	Glu	Met	Ala	Val	Leu	Asp	Ala	Glu	Leu	
58				100				105				110					
60	cgc	gcg	cat	gac	cgg	tcc	ttc	gcg	gcc	gag	ctg	ggg	tcc	act	cgc	gac	384
61	Arg	Ala	His	Asp	Arg	Ser	Phe	Ala	Ala	Glu	Leu	Gly	Ser	Thr	Arg	Asp	
62				115				120				125					
64	tcc	gtg	gcc	tgc	ggg	gtc	tgc	gtc	ggg	atc	atg	gac	tgc	atc	ccg	cac	432

ENTERED

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65 Ser Val Ala Cys Gly Val Ser Val Gly Ile Met Asp Ser Ile Pro His
66      130      135      140
68 ctg ctc gac gtc gtc ggc ggc tac ctc gac gag ggc tac gtc cgg atc      480
69 Leu Leu Asp Val Val Gly Tyr Leu Asp Glu Gly Tyr Val Arg Ile
70 145      150      155      160
72 aag ctg aag atc gag ccc ggc tgg gac gtc gag ccg gtc cgg cag gtg      528
73 Lys Leu Lys Ile Glu Pro Gly Trp Asp Val Glu Pro Val Arg Gln Val
74      165      170      175
76 cgt gag cgc ttc ggt gac gac gtg ctg ctg cag gtc gac gcg aac acc      576
77 Arg Glu Arg Phe Gly Asp Asp Val Leu Leu Gln Val Asp Ala Asn Thr
78      180      185      190
80 gcg tac acg ctg ggc gac gcg ccc ctg ctg tcc cgg ctc gac ccg ttc      624
81 Ala Tyr Thr Leu Gly Asp Ala Pro Leu Leu Ser Arg Leu Asp Pro Phe
82      195      200      205
84 gac ctg ctg ctg atc gag cag ccg ctc gaa gaa gag gac gtg ctc ggc      672
85 Asp Leu Leu Leu Ile Glu Gln Pro Leu Glu Glu Glu Asp Val Leu Gly
86      210      215      220
88 cac gcc gag ctg gcc aag cgg atc cgg acg ccg atc tgc ctc gac gag      720
89 His Ala Glu Leu Ala Lys Arg Ile Arg Thr Pro Ile Cys Leu Asp Glu
90 225      230      235      240
92 tcg atc gtc tcg gcc aag gcc gcc gcg gac gcg atc aag ctc ggc gcc      768
93 Ser Ile Val Ser Ala Lys Ala Ala Ala Asp Ala Ile Lys Leu Gly Ala
94      245      250      255
96 tgc cag atc gtc aac atc aaa ccg ggc cgg gtc ggc gga tac ctc gaa      816
97 Cys Gln Ile Val Asn Ile Lys Pro Gly Arg Val Gly Gly Tyr Leu Glu
98      260      265      270
100 gcc cgc cgg gtg cac gac gtc tgc gcg gca cac ggg atc gcg gtg tgg      864
101 Ala Arg Arg Val His Asp Val Cys Ala Ala His Gly Ile Ala Val Trp
102      275      280      285
104 tgc gcc ggg atg atc gag acc ggg ctc ggc cgg gcg gcc aac gtc gca      912
105 Cys Gly Gly Met Ile Glu Thr Gly Leu Gly Arg Ala Ala Asn Val Ala
106      290      295      300
108 ctg gcc tcg ctg ccc ggc ttc acg ctg ccg ggg gac acc tcg gcg tcc      960
109 Leu Ala Ser Leu Pro Gly Phe Thr Leu Pro Gly Asp Thr Ser Ala Ser
110 305      310      315      320
112 gcc cgg ttc tat cgc acc gac atc acc gag ccg ttc gtg ctg gac gcc      1008
113 Gly Arg Phe Tyr Arg Thr Asp Ile Thr Glu Pro Phe Val Leu Asp Ala
114      325      330      335
116 ggg cat ctg ccg gtg ccg acc ggg ccg ggc ctc ggg gtg act ccg att      1056
117 Gly His Leu Pro Val Pro Thr Gly Pro Gly Leu Gly Val Thr Pro Ile
118      340      345      350
120 ccg gat ctt ctg gac gag gtc acc acg gag aaa gcg tgg atc ggt tcg      1104
121 Pro Asp Leu Leu Asp Glu Val Thr Thr Glu Lys Ala Trp Ile Gly Ser
122      355      360      365
124 tag      1107
127 <210> SEQ ID NO: 2
128 <211> LENGTH: 368
129 <212> TYPE: PRT
130 <213> ORGANISM: Amycolatopsis orientalis

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132 &lt;400&gt; SEQUENCE: 2

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134 Val Lys Leu Ser Gly Val Glu Leu Arg Arg Val Arg Met Pro Leu Val
135 1 5 10 15
138 Ala Pro Phe Arg Thr Ser Phe Gly Thr Gln Ser Glu Arg Glu Leu Leu
139 20 25 30
142 Leu Val Arg Ala Val Thr Pro Ala Gly Glu Gly Trp Gly Glu Cys Val
143 35 40 45
146 Ala Met Glu Ala Pro Leu Tyr Ser Ser Glu Tyr Asn Asp Ala Ala Glu
147 50 55 60
150 His Val Leu Arg Asn His Leu Ile Pro Ala Leu Leu Ala Ala Glu Asp
151 65 70 75 80
154 Val Thr Ala His Lys Val Thr Pro Leu Leu Ala Lys Phe Lys Gly His
155 85 90 95
158 Arg Met Ala Lys Gly Ala Leu Glu Met Ala Val Leu Asp Ala Glu Leu
159 100 105 110
162 Arg Ala His Asp Arg Ser Phe Ala Ala Glu Leu Gly Ser Thr Arg Asp
163 115 120 125
166 Ser Val Ala Cys Gly Val Ser Val Gly Ile Met Asp Ser Ile Pro His
167 130 135 140
170 Leu Leu Asp Val Val Gly Gly Tyr Leu Asp Glu Gly Tyr Val Arg Ile
171 145 150 155 160
174 Lys Leu Lys Ile Glu Pro Gly Trp Asp Val Glu Pro Val Arg Gln Val
175 165 170 175
178 Arg Glu Arg Phe Gly Asp Asp Val Leu Leu Gln Val Asp Ala Asn Thr
179 180 185 190
182 Ala Tyr Thr Leu Gly Asp Ala Pro Leu Leu Ser Arg Leu Asp Pro Phe
183 195 200 205
186 Asp Leu Leu Leu Ile Glu Gln Pro Leu Glu Glu Glu Asp Val Leu Gly
187 210 215 220
190 His Ala Glu Leu Ala Lys Arg Ile Arg Thr Pro Ile Cys Leu Asp Glu
191 225 230 235 240
194 Ser Ile Val Ser Ala Lys Ala Ala Ala Asp Ala Ile Lys Leu Gly Ala
195 245 250 255
198 Cys Gln Ile Val Asn Ile Lys Pro Gly Arg Val Gly Gly Tyr Leu Glu
199 260 265 270
202 Ala Arg Arg Val His Asp Val Cys Ala Ala His Gly Ile Ala Val Trp
203 275 280 285
206 Cys Gly Gly Met Ile Glu Thr Gly Leu Gly Arg Ala Ala Asn Val Ala
207 290 295 300
210 Leu Ala Ser Leu Pro Gly Phe Thr Leu Pro Gly Asp Thr Ser Ala Ser
211 305 310 315 320
214 Gly Arg Phe Tyr Arg Thr Asp Ile Thr Glu Pro Phe Val Leu Asp Ala
215 325 330 335
218 Gly His Leu Pro Val Pro Thr Gly Pro Gly Leu Gly Val Thr Pro Ile
219 340 345 350
222 Pro Asp Leu Leu Asp Glu Val Thr Thr Glu Lys Ala Trp Ile Gly Ser
223 355 360 365

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## VERIFICATION SUMMARY

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Input Set : A:\ES.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date